

## SEQUENCE LISTING

<110> University of Utah Research Foundation  
Bock, Susan C.  
Hobden, Adrian N.

<120> VARIANTS OF ANTITHROMBIN III

<130> 21101.0021P1

<150> 60/384,599

<151> 2002-05-31

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<211> 54  
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&lt;220&gt;

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&lt;211&gt; 54

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<223> Description of Artificial Sequence:/note =  
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&lt;211&gt; 54

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&lt;211&gt; 54

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&lt;210&gt; 54

&lt;211&gt; 54

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

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&lt;211&gt; 54

&lt;212&gt; DNA

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<210> 61

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<210> 62

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<210> 63

<211> 54

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<210> 64

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<210> 65

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&lt;210&gt; 66

&lt;211&gt; 54

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54

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54

&lt;210&gt; 68

&lt;211&gt; 54

&lt;212&gt; DNA

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54

&lt;210&gt; 69

&lt;211&gt; 54

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

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&lt;210&gt; 70

&lt;211&gt; 430

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

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Pro Met Cys Ile Tyr Arg Ser Pro Glu Lys Lys Ala Thr Glu Asp Glu
          20          25          30
Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr Asn Arg Arg Val Trp Glu
          35          40          45
Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr Gln His Leu
          50          55          60
Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser Pro Leu Ser
65          70          75          80
Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn Asp Thr
          85          90          95
Leu Gln Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser Glu Lys
          100          105          110
Thr Ser Asp Gln Ile His Phe Phe Ala Lys Leu Asn Cys Arg Leu
          115          120          125
Tyr Arg Lys Ala Asn Lys Ala Ser Lys Leu Val Ser Ala Asn Arg Leu
          130          135          140
Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Thr Tyr Gln Asp Ile Ser
145          150          155          160
Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe Lys Glu Asn
          165          170          175
Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn Lys Thr
          180          185          190
Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn Glu Leu
          195          200          205
Thr Val Leu Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu Trp Lys
          210          215          220
Ser Lys Phe Ser Pro Glu Asn Thr Arg Lys Glu Leu Phe Tyr Lys Ala
225          230          235          240
Asp Gly Glu Ser Cys Ser Ala Ser Met Met Tyr Gln Glu Gly Lys Phe
          245          250          255
Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln Val Leu Glu Leu Pro Phe
          260          265          270
Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys Pro Glu Lys
          275          280          285
Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu Gln Glu
          290          295          300
Trp Leu Asp Glu Leu Glu Glu Met Met Leu Val Val His Met Pro Arg
305          310          315          320
Phe Arg Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln Asp Met
          325          330          335
Gly Leu Val Asp Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro Gly Ile
          340          345          350
Val Ala Glu Gly Arg Asp Asp Leu Tyr Val Ser Asp Ala Phe His Lys
          355          360          365
Ala Phe Leu Glu Val Asn Glu Glu Gly Ser Glu Ala Ala Ala Ser Thr
          370          375          380
Ala Leu Glu Ala Asn Gly Arg Ser Leu Asn Pro Asn Arg Val Thr Phe
385          390          395          400
Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro Leu Asn
          405          410          415
Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys
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synthetic construct

<400> 75  
gctgatacta acttgagggc tttgttggt tttcgatag 39

<210> 76



39

<400>	77															
Ser 1	Pro	Val	Asp	Ile 5	Cys	Thr	Ala	Lys	Pro 10	Arg	Asp	Ile	Pro	Met 15	Asn	
Pro	Met	Cys	Ile 20	Tyr	Arg	Ser	Pro	Glu 25	Lys	Lys	Ala	Thr	Glu 30	Asp	Glu	
Gly	Ser	Glu 35	Gln	Lys	Ile	Pro	Glu 40	Ala	Thr	Asn	Arg	Arg 45	Val	Trp	Glu	
Leu 50	Ser	Lys	Ala	Asn	Ser	Arg 55	Phe	Ala	Thr	Thr	Phe 60	Tyr	Gln	His	Leu	
Ala 65	Asp	Ser	Lys	Asn	Asp 70	Asn	Asp	Asn	Ile	Phe 75	Leu	Ser	Pro	Leu	Ser 80	
Ile	Ser	Thr	Ala 85	Phe	Ala	Met	Thr	Lys 90	Leu	Gly	Ala	Cys	Asn 95	Asp	Thr	
Leu	Gln	Gln 100	Leu	Met	Glu	Val	Phe	Lys 105	Phe	Asp	Thr	Ile	Ser 110	Glu	Lys	
Thr	Ser	Asp 115	Gln	Ile	His	Phe	Phe 120	Phe	Ala	Lys	Leu	Asn 125	Cys	Arg	Leu	
Tyr 130	Arg	Lys	Ala	Asn	Lys 135	Ala	Ser	Lys	Leu	Val	Ser 140	Ala	Asn	Arg	Leu	
Phe 145	Gly	Asp	Lys	Ser	Leu 150	Thr	Phe	Asn	Glu	Thr 155	Tyr	Gln	Asp	Ile	Ser 160	
Glu	Leu	Val	Tyr 165	Gly	Ala	Lys	Leu	Gln 170	Pro	Leu	Asp	Phe	Lys	Glu 175	Asn	
Ala	Glu	Gln 180	Ser	Arg	Ala	Ala	Ile	Asn 185	Lys	Trp	Val	Ser	Asn 190	Lys	Thr	
Glu	Gly	Arg 195	Ile	Thr	Asp	Val	Ile 200	Pro	Ser	Glu	Ala	Ile 205	Asn	Glu	Leu	
Thr 210	Val	Leu	Val	Leu	Val	Asn 215	Thr	Ile	Tyr	Phe	Lys 220	Gly	Leu	Trp	Lys	
Ser 225	Lys	Phe	Ser	Pro	Glu 230	Asn	Thr	Arg	Lys	Glu 235	Leu	Phe	Tyr	Lys	Ala 240	
Asp	Gly	Glu	Ser	Cys 245	Ser	Ala	Ser	Met	Met 250	Tyr	Gln	Glu	Gly	Lys 255	Phe	
Arg	Tyr	Arg	Arg 260	Val	Ala	Glu	Gly	Thr 265	Gln	Val	Leu	Glu	Leu 270	Pro	Phe	
Lys	Gly	Asp 275	Asp	Ile	Thr	Met	Val 280	Leu	Ile	Leu	Pro	Lys 285	Pro	Glu	Lys	
Ser	Leu	Ala	Lys	Val	Glu 295	Lys	Glu	Leu	Thr	Pro	Glu 300	Val	Leu	Gln	Glu	
Trp 305	Leu	Asp	Glu	Leu	Glu 310	Glu	Met	Met	Leu	Val 315	Val	His	Met	Pro	Arg 320	

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Phe Arg Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln Asp Met
      325                      330                      335
Gly Leu Val Asp Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro Gly Ile
      340                      345                      350
Val Ala Glu Gly Arg Asp Asp Leu Tyr Val Ser Asp Ala Phe His Lys
      355                      360                      365
Ala Phe Leu Glu Val Asn Glu Glu Gly Ser Glu Ala Ala Ala Ser Thr
      370                      375                      380
Ala Leu Glu Ala Gln Gly Arg Ser Leu Asn Pro Asn Arg Val Thr Phe
385                      390                      395                      400
Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro Leu Asn
      405                      410                      415
Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys
      420                      425                      430

```

&lt;210&gt; 78

&lt;211&gt; 430

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

&lt;400&gt; 78

```

Ser Pro Val Asp Ile Cys Thr Ala Lys Pro Arg Asp Ile Pro Met Asn
1      5      10      15
Pro Met Cys Ile Tyr Arg Ser Pro Glu Lys Lys Ala Thr Glu Asp Glu
20      25      30
Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr Asn Arg Arg Val Trp Glu
35      40      45
Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr Gln His Leu
50      55      60
Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser Pro Leu Ser
65      70      75      80
Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn Asp Thr
85      90      95
Leu Gln Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser Glu Lys
100     105     110
Thr Ser Asp Gln Ile His Phe Phe Phe Ala Lys Leu Asn Cys Arg Leu
115     120     125
Tyr Arg Lys Ala Asn Lys Ala Ser Lys Leu Val Ser Ala Asn Arg Leu
130     135     140
Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Thr Tyr Gln Asp Ile Ser
145     150     155     160
Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe Lys Glu Asn
165     170     175
Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn Lys Thr
180     185     190
Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn Glu Leu
195     200     205
Thr Val Leu Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu Trp Lys
210     215     220
Ser Lys Phe Ser Pro Glu Asn Thr Arg Lys Glu Leu Phe Tyr Lys Ala
225     230     235     240
Asp Gly Glu Ser Cys Ser Ala Ser Met Met Tyr Gln Glu Gly Lys Phe
245     250     255
Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln Val Leu Glu Leu Pro Phe
260     265     270
Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys Pro Glu Lys
275     280     285

```

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```

Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu Gln Glu
 290                295                300
Trp Leu Asp Glu Leu Glu Glu Met Met Leu Val Val His Met Pro Arg
305                310                315                320
Phe Arg Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln Asp Met
                325                330                335
Gly Leu Val Asp Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro Gly Ile
                340                345                350
Val Ala Glu Gly Arg Asp Asp Leu Tyr Val Ser Asp Ala Phe His Lys
                355                360                365
Ala Phe Leu Glu Val Asn Glu Glu Gly Ser Glu Ala Ala Ala Ser Thr
                370                375                380
Ala Leu Glu Ala His Gly Arg Ser Leu Asn Pro Asn Arg Val Thr Phe
385                390                395                400
Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro Leu Asn
                405                410                415
Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys
                420                425                430

```

&lt;210&gt; 79

&lt;211&gt; 1293

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

&lt;400&gt; 79

```

agccctgtgg acatctgcac agccaagccg cgggacattc ccatgaatcc catgtgcatt      60
taccgctccc cggagaagaa ggcaactgag gatgagggct cagaacagaa gatcccggag      120
gccaccaacc ggcgtgtctg ggaactgtcc aaggccaatt cccgctttgc taccactttc      180
tatcagcacc tggcagattc caagaatgac aatgataaca ttttcctgtc acccctgagt      240
atctccacgg cttttgctat gaccaagctg ggtgcctgta atgacaccct ccagcaactg      300
atggagggtat ttaagtttga caccatatct gagaaaacat ctgatcagat ccacttcttc      360
tttgccaaac tgaactgccg actctatcga aaagccaaca aagcctccaa gttagtatca      420
gccaatcgcc tttttggaga caaatccctt accttcaatg agacctacca ggacatcagt      480
gagttggtat atggagccaa gctccagccc ctggacttca aggaaaatgc agagcaatcc      540
agagcggcca tcaacaaatg ggtgtccaat aagaccgaag gccgaatcac cgatgtcatt      600
ccctcggaag ccataaatga gctcactgtt ctgggtgctg ttaacaccat ttacttcaag      660
ggcctgtgga agtcaaagtt cagccctgag aacacaagga aggaactgtt ctacaaggct      720
gatggagagt cgtgttcagc atctatgatg taccaggaag gcaagttccg ttatcggcgc      780
gtggctgaag gcacccaggt gcttgagttg cccttcaaag gtgatgacat caccatggtc      840
ctcatcttgc ccaagcctga gaagagcctg gccaaagtgg agaaggaact caccacagag      900
gtgctgcagg agtggctgga tgaattggag gagatgatgc tgggtggtoca catgccccgc      960
ttccgcattg aggacggctt cagtttgaag gagcagctgc aagacatggg ccttgctcgat      1020
ctgttcagcc ctgaaaagtc caaactccca ggtattgttg cagaaggcgc agatgacctc      1080
tatgtctcag atgcattcca taaggcattt cttgaggtaa atgaagaagg cagtgaagcg      1140
gccgcaagta ccgctotaga ggctcagggc cgttcgctaa accccaacag ggtgactttc      1200
aaggccaaca ggcctttcct ggtttttata agagaagttc ctctgaacac tattatcttc      1260
atgggcagag tagccaaccc ttgtgttaag taa                                1293

```

&lt;210&gt; 80

&lt;211&gt; 1293

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

## ATTORNEY DOCKET NO. 21101.0021P1

&lt;400&gt; 80

```

agtcccgtag atatatgcac agccaagccg cgggacattc ccatgaatcc catgtgcatt      60
taccgctccc cggagaagaa ggcaactgag gatgagggct cagaacagaa gatcccggag      120
gccaccaacc ggcgtgtctg ggaactgtcc aaggccaatt cccgctttgc taccactttc      180
tatcagcacc tggcagattc caagaatgac aatgataaca ttttcctgtc acccctgagt      240
atctccacgg cttttgctat gaccaagctg ggtgcctgta atgacaccct ccagcaactg      300
atggaggtat ttaagtttga caccatatct gagaaaacat ctgatcagat ccacttcttc      360
tttgccaaac tgaactgccg actctatcga aaagccaaca aagcctccaa gttagtatca      420
gccaatcgcc tttttggaga caaatccctt accttcaatg agacctacca ggacatcagt      480
gagttggtat atggagccaa gctccagccc ctggacttca aggaaaatgc agagcaatcc      540
agagcggcca tcaacaaatg ggtgtccaat aagaccgaag gccgaatcac cgatgtcatt      600
ccctcggaag ccatcaatga gctcactgtt ctggtgctgg ttaacaccat ttacttcaag      660
ggcctgtgga agtcaaagtt cagccctgag aacacaagga aggaactgtt ctacaaggct      720
gatggagagt cgtgttcagc atctatgatg taccaggaag gcaagttccg ttatcggcgc      780
gtggctgaag gcacccaggt gcttgagttg cccttcaaag gtgatgacat caccatggtc      840
ctcatcttgc ccaagcctga gaagagcctg gccaagggtg agaaggaact caccacagag      900
gtgctgcagg agtggtctga tgaattggag gagatgatgc tgggtggtcca catgccccgc      960
ttccgcattg aggacggctt cagtttgaag gagcagctgc aagacatggg ccttgctcgat     1020
ctgttcagcc ctgaaaagtc caaactccca ggtattgttg cagaaggccg agatgacctc     1080
tatgtctcag atgcattcca taaggcattt cttgaggtaa atgaagaagg cagtgaagcg     1140
gccgcaagta ccgctctaga ggctcagggc cgttcgctaa accccaacag ggtgactttc     1200
aaggccaaca ggcctttcct ggtttttata agagaagttc ctctgaacac tattatcttc     1260
atgggcagag tagccaaccc ttgtgttaag taa                                     1293

```

&lt;210&gt; 81

&lt;211&gt; 430

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

&lt;400&gt; 81

```

Ser Pro Val Asp Val Cys Thr Ala Lys Pro Arg Asp Ile Pro Met Asn
 1          5          10          15
Pro Met Cys Ile Tyr Arg Ser Pro Glu Lys Lys Ala Thr Glu Asp Glu
          20          25          30
Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr Asn Arg Arg Val Trp Glu
          35          40          45
Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr Gln His Leu
          50          55          60
Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser Pro Leu Ser
65          70          75          80
Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn Asp Thr
          85          90          95
Leu Gln Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser Glu Lys
          100          105          110
Thr Ser Asp Gln Ile His Phe Phe Ala Lys Leu Asn Cys Arg Leu
          115          120          125
Tyr Arg Lys Ala Asn Lys Ala Ser Lys Leu Val Ser Ala Asn Arg Leu
          130          135          140
Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Thr Tyr Gln Asp Ile Ser
145          150          155          160
Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe Lys Glu Asn
          165          170          175
Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn Lys Thr
          180          185          190
Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn Glu Leu
          195          200          205

```

## ATTORNEY DOCKET NO. 21101.0021P1

Thr	Val	Leu	Val	Leu	Val	Asn	Thr	Ile	Tyr	Phe	Lys	Gly	Leu	Trp	Lys
210						215					220				
Ser	Lys	Phe	Ser	Pro	Glu	Asn	Thr	Arg	Lys	Glu	Leu	Phe	Tyr	Lys	Ala
225					230					235					240
Asp	Gly	Glu	Ser	Cys	Ser	Ala	Ser	Met	Met	Tyr	Gln	Glu	Gly	Lys	Phe
				245					250					255	
Arg	Tyr	Arg	Arg	Val	Ala	Glu	Gly	Thr	Gln	Val	Leu	Glu	Leu	Pro	Phe
			260					265					270		
Lys	Gly	Asp	Asp	Ile	Thr	Met	Val	Leu	Ile	Leu	Pro	Lys	Pro	Glu	Lys
		275					280					285			
Ser	Leu	Ala	Lys	Val	Glu	Lys	Glu	Leu	Thr	Pro	Glu	Val	Leu	Gln	Glu
	290					295					300				
Trp	Leu	Asp	Glu	Leu	Glu	Glu	Met	Met	Leu	Val	Val	His	Met	Pro	Arg
305					310					315					320
Phe	Arg	Ile	Glu	Asp	Gly	Phe	Ser	Leu	Lys	Glu	Gln	Leu	Gln	Asp	Met
				325					330					335	
Gly	Leu	Val	Asp	Leu	Phe	Ser	Pro	Glu	Lys	Ser	Lys	Leu	Pro	Gly	Ile
			340					345					350		
Val	Ala	Glu	Gly	Arg	Asp	Asp	Leu	Tyr	Val	Ser	Asp	Ala	Phe	His	Lys
	355						360					365			
Ala	Phe	Leu	Glu	Val	Asn	Glu	Glu	Gly	Ser	Glu	Ala	Ala	Ala	Ser	Thr
	370					375					380				
Ala	Leu	Glu	Ala	Gln	Gly	Arg	Ser	Leu	Asn	Pro	Asn	Arg	Val	Thr	Phe
385					390					395					400
Lys	Ala	Asn	Arg	Pro	Phe	Leu	Val	Phe	Ile	Arg	Glu	Val	Pro	Leu	Asn
				405					410					415	
Thr	Ile	Ile	Phe	Met	Gly	Arg	Val	Ala	Asn	Pro	Cys	Val	Lys		
			420					425					430		

&lt;210&gt; 82

&lt;211&gt; 1293

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

&lt;400&gt; 82

agccctgtgg	acgtatgcac	agccaagccg	cgggacattc	ccatgaatcc	catgtgcatt	60
taccgctccc	cggagaagaa	ggcaactgag	gatgagggct	cagaacagaa	gatcccggag	120
gccaccaacc	ggcgtgtctg	ggaactgtcc	aaggccaatt	cccgctttgc	taccactttc	180
tatcagcacc	tggcagattc	caagaatgac	aatgataaca	ttttcctgtc	acctctgagt	240
atctccacgg	cttttgctat	gaccaagctg	ggtgcctgta	atgacaccct	ccagcaactg	300
atggagggtat	ttaagtttga	caccatatct	gagaaaacat	ctgatcagat	ccacttcttc	360
tttgccaaac	tgaactgccg	actctatcga	aaagccaaca	aagcctccaa	gttagtatca	420
gccaatcgcc	tttttgagga	caaatccctt	accttcaatg	agacctacca	ggacatcagt	480
gagttggtat	atggagccaa	gctccagccc	ctggacttca	aggaaaatgc	agagcaatcc	540
agagcggcca	tcaacaaatg	ggtgtccaat	aagaccgaag	gccgaatcac	cgatgtcatt	600
ccctcggaag	ccatcaatga	gtcactgttt	ctgggtgctgg	ttaacaccat	ttacttcaag	660
ggcctgtgga	agtcaaaagt	cagccctgag	aacacaagga	aggaactgtt	ctacaaggct	720
gatggagagt	cgtgttcagc	atctatgatg	taccaggaag	gcaagttccg	ttatcggcgc	780
gtggctgaag	gcacccaggt	gcttgagttg	cccttcaaag	gtgatgacat	caccatggtc	840
ctcatcttgc	ccaagcctga	gaagagcctg	gccaagggtg	agaagggaact	caccccagag	900
gtgctgcagg	agtggctgga	tgaattggag	gagatgatgc	tggtggtcca	catgccccgc	960
ttccgcattg	aggacggctt	cagtttgaag	gagcagctgc	aagacatggg	ccttgtcgat	1020
ctgttcagcc	ctgaaaagtc	caaactccca	ggtattgttg	cagaaggccg	agatgacctc	1080
tatgtctcag	atgcattcca	taaggcattt	cttgaggtaa	atgaagaagg	cagtgaagcg	1140
gccgcaagta	ccgctctaga	ggctcagggc	cgctcgctaa	acccaacag	ggtgactttc	1200
aaggccaaca	ggcctttcct	ggtttttata	agagaagttc	ctctgaacac	tattatcttc	1260
atgggcagag	tagccaaccc	ttgtgttaag	taa			1293

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<210> 83  
 <211> 1293  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:/note =  
 synthetic construct

<400> 83  
 agtcccgtag atgtgtgcac agccaagccg cgggacattc ccatgaatcc catgtgcatt 60  
 taccgctccc cggagaagaa ggcaactgag gatgagggtc cagaacagaa gatcccggag 120  
 gccaccaacc ggcgtgtctg ggaactgtcc aaggccaatt cccgctttgc taccactttc 180  
 tatcagcacc tggcagattc caagaatgac aatgataaca ttttcctgtc acccctgagt 240  
 atctccacgg cttttgctat gaccaagctg ggtgcctgta atgacaccct ccagcaactg 300  
 atggagggtat ttaagtttga caccatatct gagaaaacat ctgacagat ccacttcttc 360  
 tttgccaaac tgaactgccg actctatcga aaagccaaca aagcctccaa gttagtatca 420  
 gccaatcgcc tttttggaga caaatccctt accttcaatg agacctacca ggacatcagt 480  
 gatttggtat atggagccaa gctccagccc ctggacttca aggaaaatgc agagcaatcc 540  
 agagcggcca tcaacaaatg ggtgtccaat aagaccgaag gccgaatcac cgatgtcatt 600  
 ccctcggaag ccatcaatga gctcactgtt ctggtgctgg ttaacaccat ttacttcaag 660  
 ggcctgtgga agtcaaagtt cagccctgag aacacaagga aggaactgtt ctacaaggct 720  
 gatggagagt cgtgttcagc atctatgatg taccaggaag gcaagttccg ttatcggcgc 780  
 gtggctgaag gcacccaggt gcttgagttg cccttcaaag gtgatgacat caccatggtc 840  
 ctcactttgc ccaagcctga gaagagcctg gccaagggtg agaaggaact caccacagag 900  
 gtgctgcagg agtggtctga tgaattggag gagatgatgc tgggtgtcca catgccccgc 960  
 ttccgcattg aggacggctt cagtttgaag gagcagctgc aagacatggg ccttgtcgat 1020  
 ctgttcagcc ctgaaaagtc caaactccca ggtattgttg cagaaggccg agatgacctc 1080  
 tatgtctcag atgcattcca taaggcattt cttgaggtaa atgaagaagg cagtgaagcg 1140  
 gccgcaagta ccgctctaga ggctcagggc cgttcgctaa accccaacag ggtgactttc 1200  
 aaggccaaca ggcctttcct ggtttttata agagaagttc ctctgaacac tattatcttc 1260  
 atgggcagag tagccaaccc ttgtgttaag taa 1293

<210> 84  
 <211> 430  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:/note =  
 synthetic construct

<400> 84  
 Ser Pro Val Asp Ile Cys Thr Ala Lys Pro Arg Asp Ile Pro Met Asn  
 1 5 10 15  
 Pro Met Cys Ile Tyr Arg Ser Pro Glu Lys Lys Ala Thr Glu Asp Glu  
 20 25 30  
 Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr Asn Arg Arg Val Trp Glu  
 35 40 45  
 Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr Gln His Leu  
 50 55 60  
 Ala Asp Ser Lys Asn Asp Asn Ile Phe Leu Ser Pro Leu Ser  
 65 70 75 80  
 Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn Asp Thr  
 85 90 95  
 Leu Gln Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser Glu Lys  
 100 105 110  
 Thr Ser Asp Gln Ile His Phe Phe Ala Lys Leu Asn Cys Arg Leu  
 115 120 125

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```

Tyr Arg Lys Ala Asn Lys Ala Ser Lys Leu Val Ser Ala Asn Arg Leu
 130                      135                      140
Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Thr Tyr Gln Asp Ile Ser
145                      150                      155                      160
Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe Lys Glu Asn
                      165                      170                      175
Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn Lys Thr
                      180                      185                      190
Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn Glu Leu
                      195                      200                      205
Thr Val Leu Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu Trp Lys
                      210                      215                      220
Ser Lys Phe Ser Pro Glu Asn Thr Arg Lys Glu Leu Phe Tyr Lys Ala
225                      230                      235                      240
Asp Gly Glu Ser Cys Ser Ala Ser Met Met Tyr Gln Glu Gly Lys Phe
                      245                      250                      255
Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln Val Leu Glu Leu Pro Phe
                      260                      265                      270
Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys Pro Glu Lys
                      275                      280                      285
Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu Gln Glu
290                      295                      300
Trp Leu Asp Glu Leu Glu Glu Met Met Leu Val Val His Met Pro Arg
305                      310                      315                      320
Phe Arg Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln Asp Met
                      325                      330                      335
Gly Leu Val Asp Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro Gly Ile
                      340                      345                      350
Val Ala Glu Gly Arg Asp Asp Leu Tyr Val Ser Asp Ala Phe His Lys
                      355                      360                      365
Ala Phe Leu Glu Val Asn Glu Glu Gly Ser Glu Ala Ala Ala Ser Thr
                      370                      375                      380
Ala Leu Glu Ala Tyr Gly Arg Ser Leu Asn Pro Asn Arg Val Thr Phe
385                      390                      395                      400
Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro Leu Asn
                      405                      410                      415
Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys
                      420                      425                      430

```

&lt;210&gt; 85

&lt;211&gt; 432

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

&lt;400&gt; 85

```

His Gly Ser Pro Val Asp Ile Cys Thr Ala Lys Pro Arg Asp Ile Pro
 1                      5                      10                      15
Met Asn Pro Met Cys Ile Tyr Arg Ser Pro Glu Lys Lys Ala Thr Glu
                      20                      25                      30
Asp Glu Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr Asn Arg Arg Val
                      35                      40                      45
Trp Glu Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr Gln
50                      55                      60
His Leu Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser Pro
65                      70                      75                      80
Leu Ser Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn
                      85                      90                      95

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## ATTORNEY DOCKET NO. 21101.0021P1

```

Asp Thr Leu Gln Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser
      100      105      110
Glu Lys Thr Ser Asp Gln Ile His Phe Phe Phe Ala Lys Leu Asn Cys
      115      120      125
Arg Leu Tyr Arg Lys Ala Asn Lys Ser Ser Lys Leu Val Ser Ala Asn
      130      135      140
Arg Leu Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Thr Tyr Gln Asp
145      150      155      160
Ile Ser Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe Lys
      165      170      175
Glu Asn Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn
      180      185      190
Lys Thr Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn
      195      200      205
Glu Leu Thr Val Leu Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu
210      215      220
Trp Lys Ser Lys Phe Ser Pro Glu Asn Thr Arg Lys Glu Leu Phe Tyr
225      230      235      240
Lys Ala Asp Gly Glu Ser Cys Ser Ala Ser Met Met Tyr Gln Glu Gly
      245      250      255
Lys Phe Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln Val Leu Glu Leu
      260      265      270
Pro Phe Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys Pro
      275      280      285
Glu Lys Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu
290      295      300
Gln Glu Trp Leu Asp Glu Leu Glu Glu Met Met Leu Val Val His Met
305      310      315      320
Pro Arg Phe Arg Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln
      325      330      335
Asp Met Gly Leu Val Asp Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro
      340      345      350
Gly Ile Val Ala Glu Gly Arg Asp Asp Leu Tyr Val Ser Asp Ala Phe
      355      360      365
His Lys Ala Phe Leu Glu Val Asn Glu Glu Gly Ser Glu Ala Ala Ala
      370      375      380
Ser Thr Ala Leu Glu Ala Gln Gly Arg Ser Leu Asn Pro Asn Arg Val
385      390      395      400
Thr Phe Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro
      405      410      415
Leu Asn Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys
      420      425      430

```

&lt;210&gt; 86

&lt;211&gt; 432

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

&lt;400&gt; 86

```

His Gly Ser Pro Val Asp Ile Cys Thr Ala Lys Pro Arg Asp Ile Pro
 1      5      10      15
Met Asn Pro Met Cys Ile Tyr Arg Ser Pro Glu Lys Lys Ala Thr Glu
      20      25      30
Asp Glu Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr Asn Arg Arg Val
      35      40      45

```



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```

Trp Glu Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr Gln
  50          55          60
His Leu Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser Pro
  65          70          75          80
Leu Ser Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn
          85          90          95
Asp Thr Leu Gln Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser
          100          105          110
Glu Lys Thr Ser Asp Gln Ile His Phe Phe Phe Ala Lys Leu Asn Cys
          115          120          125
Arg Leu Tyr Arg Lys Ala Asn Lys Ser Ser Lys Leu Val Ser Ala Asn
          130          135          140
Arg Leu Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Thr Tyr Gln Asp
          145          150          155          160
Ile Ser Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe Lys
          165          170          175
Glu Asn Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn
          180          185          190
Lys Thr Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn
          195          200          205
Glu Leu Thr Val Leu Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu
          210          215          220
Trp Lys Ser Lys Phe Ser Pro Glu Asn Thr Arg Lys Glu Leu Phe Tyr
          225          230          235          240
Lys Ala Asp Gly Glu Ser Cys Ser Ala Ser Met Met Tyr Gln Glu Gly
          245          250          255
Lys Phe Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln Val Leu Glu Leu
          260          265          270
Pro Phe Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys Pro
          275          280          285
Glu Lys Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu
          290          295          300
Gln Glu Trp Leu Asp Glu Leu Glu Glu Met Met Leu Val Val His Met
          305          310          315          320
Pro Arg Phe Arg Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln
          325          330          335
Asp Met Gly Leu Val Asp Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro
          340          345          350
Gly Ile Val Ala Glu Gly Arg Asp Asp Leu Tyr Val Ser Asp Ala Phe
          355          360          365
His Lys Ala Phe Leu Glu Val Asn Glu Glu Gly Ser Glu Ala Ala Ala
          370          375          380
Ser Thr Ala Leu Glu Ala His Gly Arg Ser Leu Asn Pro Asn Arg Val
          385          390          395          400
Thr Phe Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro
          405          410          415
Leu Asn Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys
          420          425          430

```

&lt;210&gt; 87

&lt;211&gt; 432

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

&lt;400&gt; 87

```

His Gly Ser Pro Val Asp Ile Cys Thr Ala Lys Pro Arg Asp Ile Pro
  1          5          10          15

```

## ATTORNEY DOCKET NO. 21101.0021P1

Met	Asn	Pro	Met	Cys	Ile	Tyr	Arg	Ser	Pro	Glu	Lys	Lys	Ala	Thr	Glu
			20					25					30		
Asp	Glu	Gly	Ser	Glu	Gln	Lys	Ile	Pro	Glu	Ala	Thr	Asn	Arg	Arg	Val
		35				40						45			
Trp	Glu	Leu	Ser	Lys	Ala	Asn	Ser	Arg	Phe	Ala	Thr	Thr	Phe	Tyr	Gln
		50				55					60				
His	Leu	Ala	Asp	Ser	Lys	Asn	Asp	Asn	Asp	Asn	Ile	Phe	Leu	Ser	Pro
65					70					75					80
Leu	Ser	Ile	Ser	Thr	Ala	Phe	Ala	Met	Thr	Lys	Leu	Gly	Ala	Cys	Asn
				85					90					95	
Asp	Thr	Leu	Gln	Gln	Leu	Met	Glu	Val	Phe	Lys	Phe	Asp	Thr	Ile	Ser
			100					105					110		
Glu	Lys	Thr	Ser	Asp	Gln	Ile	His	Phe	Phe	Phe	Ala	Lys	Leu	Asn	Cys
		115				120						125			
Arg	Leu	Tyr	Arg	Lys	Ala	Asn	Lys	Ser	Ser	Lys	Leu	Val	Ser	Ala	Asn
		130				135						140			
Arg	Leu	Phe	Gly	Asp	Lys	Ser	Leu	Thr	Phe	Asn	Glu	Thr	Tyr	Gln	Asp
145					150					155					160
Ile	Ser	Glu	Leu	Val	Tyr	Gly	Ala	Lys	Leu	Gln	Pro	Leu	Asp	Phe	Lys
				165					170					175	
Glu	Asn	Ala	Glu	Gln	Ser	Arg	Ala	Ala	Ile	Asn	Lys	Trp	Val	Ser	Asn
			180					185					190		
Lys	Thr	Glu	Gly	Arg	Ile	Thr	Asp	Val	Ile	Pro	Ser	Glu	Ala	Ile	Asn
		195				200						205			
Glu	Leu	Thr	Val	Leu	Val	Leu	Val	Asn	Thr	Ile	Tyr	Phe	Lys	Gly	Leu
		210				215						220			
Trp	Lys	Ser	Lys	Phe	Ser	Pro	Glu	Asn	Thr	Arg	Lys	Glu	Leu	Phe	Tyr
225					230					235					240
Lys	Ala	Asp	Gly	Glu	Ser	Cys	Ser	Ala	Ser	Met	Met	Tyr	Gln	Glu	Gly
			245						250					255	
Lys	Phe	Arg	Tyr	Arg	Arg	Val	Ala	Glu	Gly	Thr	Gln	Val	Leu	Glu	Leu
			260					265					270		
Pro	Phe	Lys	Gly	Asp	Asp	Ile	Thr	Met	Val	Leu	Ile	Leu	Pro	Lys	Pro
		275				280						285			
Glu	Lys	Ser	Leu	Ala	Lys	Val	Glu	Lys	Glu	Leu	Thr	Pro	Glu	Val	Leu
		290				295					300				
Gln	Glu	Trp	Leu	Asp	Glu	Leu	Glu	Glu	Met	Met	Leu	Val	Val	His	Met
305					310					315					320
Pro	Arg	Phe	Arg	Ile	Glu	Asp	Gly	Phe	Ser	Leu	Lys	Glu	Gln	Leu	Gln
				325					330					335	
Asp	Met	Gly	Leu	Val	Asp	Leu	Phe	Ser	Pro	Glu	Lys	Ser	Lys	Leu	Pro
			340					345					350		
Gly	Ile	Val	Ala	Glu	Gly	Arg	Asp	Asp	Leu	Tyr	Val	Ser	Asp	Ala	Phe
		355				360						365			
His	Lys	Ala	Phe	Leu	Glu	Val	Asn	Glu	Glu	Gly	Ser	Glu	Ala	Ala	Ala
		370				375					380				
Ser	Thr	Ala	Leu	Glu	Ala	Tyr	Gly	Arg	Ser	Leu	Asn	Pro	Asn	Arg	Val
385					390					395					400
Thr	Phe	Lys	Ala	Asn	Arg	Pro	Phe	Leu	Val	Phe	Ile	Arg	Glu	Val	Pro
			405					410					415		
Leu	Asn	Thr	Ile	Ile	Phe	Met	Gly	Arg	Val	Ala	Asn	Pro	Cys	Val	Lys
			420					425					430		

&lt;210&gt; 88

&lt;211&gt; 423

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:/note =

ATTORNEY DOCKET NO. 21101.0021P1

synthetic construct

&lt;400&gt; 88

```

Arg Asp Ile Pro Val Asn Pro Ile Cys Ile Tyr Arg Asn Pro Glu Lys
 1          5          10          15
Lys Pro Gln Glu Arg Arg Gly Ala Gly Ala Gly Glu Gly Gln Asp Pro
 20          25          30
Gly Val His Lys Pro Pro Val Trp Glu Leu Ser Arg Ala Asn Ser Arg
 35          40          45
Phe Ala Val Val Phe Tyr Lys His Leu Ala Asp Ser Lys Asp Asn Glu
 50          55          60
Glu Asn Ile Phe Leu Ser Pro Leu Ser Ile Ser Thr Ala Phe Ala Met
 65          70          75          80
Thr Lys Leu Gly Ala Cys Gly Asp Thr Leu Gln Gln Leu Met Glu Val
 85          90          95
Phe Gln Phe Asp Thr Ile Ser Glu Lys Thr Ser Asp Gln Val His Phe
100          105          110
Phe Phe Ala Lys Leu Asn Cys Arg Leu Tyr Lys Lys Ala Asn Lys Ser
115          120          125
Ser Glu Leu Ile Ser Ala Asn Arg Leu Phe Gly Glu Lys Ser Leu Val
130          135          140
Phe Asn Glu Thr Tyr Gln Asn Ile Ser Glu Ile Val Tyr Gly Ala Lys
145          150          155          160
Leu Trp Pro Leu Asn Phe Lys Glu Lys Pro Glu Leu Ser Arg Lys Ile
165          170          175
Ile Asn Glu Trp Val Ala Asn Lys Thr Glu Arg Arg Ile Thr Glu Val
180          185          190
Ile Pro Glu Lys Gly Ile Asp Asp Leu Thr Val Leu Val Leu Val Asn
195          200          205
Thr Ile Tyr Phe Lys Gly His Trp Lys Ser Gln Phe Pro Ala Pro Asn
210          215          220
Thr Arg Leu Asp Leu Phe His Lys Ala Asn Gly Glu Thr Cys Asn Val
225          230          235          240
Pro Ile Met Tyr Gln Glu Ser Arg Phe Pro Tyr Ala Phe Ile Gln Glu
245          250          255
Asp Lys Val Gln Val Leu Glu Leu Pro Tyr Lys Gly Asp Asp Ile Thr
260          265          270
Met Val Leu Val Leu Pro Lys Ala Gly Thr Pro Leu Val Glu Val Glu
275          280          285
Arg Asp Leu Thr Ser Asp Lys Leu Gln Asp Trp Ile Asp Ser Met Met
290          295          300
Glu Val Ser Leu Thr Val Ser Phe Pro Arg Phe Arg Val Glu Asp Ser
305          310          315          320
Phe Ser Val Lys Glu Lys Leu Arg Lys Met Gly Leu Glu Asp Leu Phe
325          330          335
Ser Pro Glu Asn Ala Lys Leu Pro Gly Ile Val Ala Gly Asp Arg Thr
340          345          350
Asp Leu Tyr Val Ser Glu Ala Phe His Lys Ala Phe Leu Glu Val Asn
355          360          365
Glu Glu Gly Ser Glu Ala Ser Ala Ala Thr Ala Val Val Ile Ser Gly
370          375          380
Arg Ser Phe Pro Met Asn Arg Ile Ile Phe Glu Ala Asn Arg Pro Phe
385          390          395          400
Leu Leu Phe Ile Arg Glu Ala Thr Leu Asn Thr Ile Ile Phe Met Gly
405          410          415
Arg Ile Ser Asp Pro Cys Ser
420

```

&lt;210&gt; 89

&lt;211&gt; 456

## ATTORNEY DOCKET NO. 21101.0021P1

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

&lt;400&gt; 89

```

Met Tyr Leu Leu Ser Leu Leu Leu Leu Ser Leu Leu Gly Ser Ala Tyr
 1          5          10          15
Leu Gln Pro Gln His Ala Asp Ile Cys Leu Ala Lys Pro Lys Asp Ile
          20          25          30
Pro Leu Thr Pro Met Cys Val Tyr Arg Lys Pro Leu Glu Val Val Glu
          35          40          45
Thr Glu Glu Lys Glu Lys Glu Pro Thr Thr Gln Glu Lys Val Pro
          50          55          60
Glu Ser Thr Asn Pro Arg Val Tyr Glu Leu Ser Gln Ala Asn Ala Lys
65          70          75          80
Phe Ala Ile Ala Phe Tyr Lys Asn Leu Ala Asp Ser Lys Arg Asp Lys
          85          90          95
Glu Asn Ile Phe Met Ser Pro Leu Ser Ile Ser Gln Ala Phe Thr Met
          100          105          110
Ala Lys Leu Gly Ala Cys Asn Asn Thr Leu Lys Gln Leu Met Glu Val
          115          120          125
Phe His Phe Asp Thr Val Ser Glu Arg Ala Ser Asp Gln Ile His Tyr
130          135          140
Phe Phe Ala Lys Leu Asn Cys Arg Leu Phe Arg Lys Ala Asn Lys Ser
145          150          155          160
Ser Glu Leu Val Ser Val Asn Arg Leu Phe Gly Glu Lys Ser Leu Thr
          165          170          175
Phe Asn Glu Thr Tyr Gln Asp Ile Ser Glu Ile Val Tyr Gly Ala Lys
          180          185          190
Leu Trp Pro Leu Asn Phe Arg Asp Lys Pro Glu Leu Ser Arg Glu Ile
          195          200          205
Ile Asn Asn Trp Val Ser Asn Lys Thr Glu Lys Arg Ile Thr Asp Val
210          215          220
Ile Pro Lys Asp Ala Ile Thr Pro Asp Thr Val Leu Val Leu Ile Asn
225          230          235          240
Ala Ile Tyr Phe Lys Gly Leu Trp Lys Ser Lys Phe Asn Ser Glu Asn
          245          250          255
Thr Lys Met Asp Gln Phe His Pro Ala Lys Asn Ser Asn Cys Leu Thr
          260          265          270
Ala Thr Met Tyr Gln Glu Gly Thr Phe Arg Tyr Gly Ser Phe Lys Asp
          275          280          285
Asp Gly Val Gln Val Leu Glu Leu Pro Tyr Lys Gly Asp Asp Ile Thr
290          295          300
Met Val Leu Val Leu Pro Ser Gln Glu Thr Pro Leu Thr Thr Val Glu
305          310          315          320
Gln Asn Leu Thr Leu Glu Lys Leu Gly Asn Trp Leu Gln Lys Ser Arg
          325          330          335
Glu Leu Gln Leu Ser Val Tyr Leu Pro Arg Phe Arg Val Glu Asp Ser
          340          345          350
Phe Ser Val Lys Glu Lys Leu Gln Glu Met Gly Leu Val Asp Leu Phe
          355          360          365
Asp Pro Asn Ser Ala Lys Leu Pro Gly Ile Ile Ala Gly Gly Arg Thr
          370          375          380
Asp Leu Tyr Val Ser Asp Ala Phe His Lys Ala Phe Leu Glu Val Asn
385          390          395          400
Glu Glu Gly Ser Glu Ala Ala Ala Ser Thr Ala Val Ile Leu Thr Gly
          405          410          415

```

## ATTORNEY DOCKET NO. 21101.0021P1

Arg Ser Leu Asn Leu Asn Arg Ile Ile Phe Arg Ala Asn Arg Pro Phe  
                   420                  425                  430  
 Leu Val Phe Ile Arg Glu Val Ala Ile Asn Ala Ile Leu Phe Met Gly  
                   435                  440                  445  
 Arg Val Ala Asn Pro Cys Thr Glu  
           450                  455

&lt;210&gt; 90

&lt;211&gt; 465

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
       synthetic construct

&lt;400&gt; 90

Met Tyr Ser Pro Gly Ala Gly Ser Gly Ala Ala Gly Glu Arg Lys Leu  
   1                  5                  10                  15  
 Cys Leu Leu Ser Leu Leu Leu Ile Gly Ala Leu Gly Cys Ala Ile Cys  
                   20                  25                  30  
 His Gly Asn Pro Val Asp Asp Ile Cys Ile Ala Lys Pro Arg Asp Ile  
           35                  40                  45  
 Pro Val Asn Pro Leu Cys Ile Tyr Arg Ser Pro Gly Lys Lys Ala Thr  
   50                  55                  60  
 Glu Glu Asp Gly Ser Glu Gln Lys Val Pro Glu Ala Thr Asn Arg Arg  
  65                  70                  75                  80  
 Val Trp Glu Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Asn Phe Tyr  
                   85                  90                  95  
 Gln His Leu Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser  
          100                 105                 110  
 Pro Leu Ser Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys  
  115                 120                 125  
 Asn Asp Thr Leu Lys Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile  
  130                 135                 140  
 Ser Glu Lys Thr Ser Asp Gln Ile His Phe Phe Phe Ala Lys Leu Asn  
  145                 150                 155                 160  
 Cys Arg Leu Tyr Arg Lys Ala Asn Lys Ser Ser Asp Leu Val Ser Ala  
                  165                 170                 175  
 Asn Arg Leu Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Ser Tyr Gln  
          180                 185                 190  
 Asp Val Ser Glu Val Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe  
  195                 200                 205  
 Lys Glu Asn Pro Glu Gln Ser Arg Val Thr Ile Asn Asn Trp Val Ala  
  210                 215                 220  
 Asn Lys Thr Glu Gly Arg Ile Lys Asp Val Ile Pro Gln Gly Ala Ile  
  225                 230                 235                 240  
 Asn Glu Leu Thr Ala Leu Val Leu Val Asn Thr Ile Tyr Phe Lys Gly  
                  245                 250                 255  
 Leu Trp Lys Ser Lys Phe Ser Pro Glu Asn Thr Arg Lys Glu Pro Phe  
          260                 265                 270  
 Tyr Lys Val Asp Gly Gln Ser Cys Pro Val Pro Met Met Tyr Gln Glu  
          275                 280                 285  
 Gly Lys Phe Lys Tyr Arg Arg Val Ala Glu Gly Thr Gln Val Leu Glu  
  290                 295                 300  
 Leu Pro Phe Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys  
  305                 310                 315                 320  
 Pro Glu Lys Ser Leu Ala Lys Val Glu Gln Glu Leu Thr Pro Glu Leu  
                  325                 330                 335  
 Leu Gln Glu Trp Leu Asp Glu Leu Ser Glu Thr Met Leu Val Val His  
          340                 345                 350

## ATTORNEY DOCKET NO. 21101.0021P1

Met Pro Arg Phe Arg Thr Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu  
                   355                                  360                                  365  
 Gln Asp Met Gly Leu Ile Asp Leu Phe Ser Pro Glu Lys Ser Gln Leu  
                   370                                  375                                  380  
 Pro Gly Ile Val Ala Gly Gly Arg Asp Asp Leu Tyr Val Ser Asp Ala  
 385                                  390                                  395                                  400  
 Phe His Lys Ala Phe Leu Glu Val Asn Glu Gly Ser Glu Ala Ala  
                                   405                                  410                                  415  
 Ala Ser Thr Ser Val Val Ile Thr Gly Arg Ser Leu Asn Pro Asn Arg  
                                   420                                  425                                  430  
 Val Thr Phe Lys Ala Asn Arg Pro Phe Leu Val Leu Ile Arg Glu Val  
                                   435                                  440                                  445  
 Ala Leu Asn Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val  
                                   450                                  455                                  460  
 Asn  
 465

&lt;210&gt; 91

&lt;211&gt; 1599

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
 synthetic construct

&lt;400&gt; 91

caccagcattc	atctcctcca	attcatccag	ctactctgcc	catgaagata	atagttttca	60
ggcggattgc	ctcagatcac	actatctcca	cttgcccagc	cctgtggaag	attagcggcc	120
atgtattcca	atgtgatagg	aactgtaacc	tctggaaaaa	ggaagggtta	tcttttgtcc	180
ttgctgctca	ttggcttctg	ggactgctg	acctgtcaag	ggagccctgt	ggacatctgc	240
acagccaagc	cgcgggacat	tcccatgaat	cccatgtgca	tttaccgctc	cccggagaag	300
aaggcaactg	aggatgaggg	ctcagaacag	aagatcccgg	aggccacca	ccggcgtgtc	360
tgggaactgt	ccaaggccaa	ttcccgttt	gctaccactt	tctatcagca	cctggcagat	420
tccaagaatg	acaatgataa	cattttcctg	tcacccctga	gtatctccac	ggcttttgc	480
atgaccaagc	tgggtgcctg	taatgacacc	ctccagcaac	tgatggaggt	atttaagttt	540
gacaccatat	ctgagaaaac	atctgatcag	atccacttct	tctttgccaa	actgaactgc	600
cgactctatc	gaaaagccaa	caaatcctcc	aagttagtag	cagccaatcg	cctttttgga	660
gacaaatccc	ttaccttcaa	tgagacctac	caggacatca	gtgagttgg	atatggagcc	720
aagctccagc	ccctggactt	caaggaaaat	gcagagcaat	ccagagcggc	catcaacaaa	780
tgggtgtcca	ataagaccga	aggccgaatc	accgatgtca	ttccctcgga	agccatcaat	840
gagctcactg	ttctggtgct	ggttaacacc	atttacttca	agggcctgtg	gaagtcaaag	900
ttcagccctg	agaacacaag	gaaggaaactg	ttctacaagg	ctgatggaga	gtcgtgttca	960
gcatctatga	tgtaccagga	aggcaagttc	cgttatcggc	gcgtggctga	aggcaccag	1020
gtgcttgagt	tgcccttcaa	aggtgatgac	atcaccatgg	tcctcatctt	gccaagcct	1080
gagaagagcc	tggccaaggt	ggagaaggaa	ctcaccocag	aggtgctgca	ggagtggctg	1140
gatgaattgg	aggagatgat	gctgggtggt	cacatgcccc	gcttccgcat	tgaggacggc	1200
ttcagtttga	aggagcagct	gcaagacatg	ggccttgctg	atctgttcag	ccctgaaaag	1260
tccaaactcc	caggtattgt	tgacagaaggc	cgagatgacc	tctatgtctc	agatgcattc	1320
cataaggcat	ttcttgaggt	aaatgaagaa	ggcagtgaag	cagctgcaag	taccgctgtt	1380
gtgattgctg	gccgttcgct	aaaccccaac	agggtagact	tcaaggccaa	caggcccttc	1440
ctgggtttta	taagagaagt	tcctctgaac	actattatct	tcatgggcag	agtagccaac	1500
ccttggtgta	agtaaaatgt	tcttattctt	tgcacctctt	cctatttttg	gtttgtgaac	1560
agaagtaaaa	ataaatacaa	actacttcca	tctcacatt			1599

&lt;210&gt; 92

&lt;211&gt; 430

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Xaa = any amino acid

1001	Pro	Val	Asp	Ile	Cys	Thr	Ala	Lys	Pro	Arg	Asp	Ile	Pro	Met	Asn
1	Pro	Met	Cys	Ile	Tyr	Arg	Ser	Pro	Glu	Lys	Lys	Ala	Thr	Glu	Asp
			20						25					30	
	Gly	Ser	Glu	Gln	Lys	Ile	Pro	Glu	Ala	Thr	Asn	Arg	Arg	Val	Trp
			35					40					45		
	Leu	Ser	Lys	Ala	Asn	Ser	Arg	Phe	Ala	Thr	Thr	Phe	Tyr	Gln	His
		50					55					60			Leu
	Ala	Asp	Ser	Lys	Asn	Asp	Asn	Asp	Asn	Ile	Phe	Leu	Ser	Pro	Leu
	65					70					75				80
	Ile	Ser	Thr	Ala	Phe	Ala	Met	Thr	Lys	Leu	Gly	Ala	Cys	Asn	Asp
				85						90					95
	Leu	Gln	Gln	Leu	Met	Glu	Val	Phe	Lys	Phe	Asp	Thr	Ile	Ser	Glu
			100						105					110	Lys
	Thr	Ser	Asp	Gln	Ile	His	Phe	Phe	Phe	Ala	Lys	Leu	Asn	Cys	Arg
			115					120					125		Leu
	Tyr	Arg	Lys	Ala	Asn	Lys	Ala	Ser	Lys	Leu	Val	Ser	Ala	Asn	Arg
		130					135					140			Leu
	Phe	Gly	Asp	Lys	Ser	Leu	Thr	Phe	Asn	Glu	Thr	Tyr	Gln	Asp	Ile
	145					150					155				160
	Glu	Leu	Val	Tyr	Gly	Ala	Lys	Leu	Gln	Pro	Leu	Asp	Phe	Lys	Glu
				165						170					175
	Ala	Glu	Gln	Ser	Arg	Ala	Ala	Ile	Asn	Lys	Trp	Val	Ser	Asn	Lys
			180						185					190	Thr
	Glu	Gly	Arg	Ile	Thr	Asp	Val	Ile	Pro	Ser	Glu	Ala	Ile	Asn	Glu
			195					200					205		Leu
	Thr	Val	Leu	Val	Leu	Val	Asn	Thr	Ile	Tyr	Phe	Lys	Gly	Leu	Trp
		210					215					220			Lys
	Ser	Lys	Phe	Ser	Pro	Glu	Asn	Thr	Arg	Lys	Glu	Leu	Phe	Tyr	Lys
	225					230					235				Ala
	Asp	Gly	Glu	Ser	Cys	Ser	Ala	Ser	Met	Met	Tyr	Gln	Glu	Gly	Lys
				245						250					255
	Arg	Tyr	Arg	Arg	Val	Ala	Glu	Gly	Thr	Gln	Val	Leu	Glu	Leu	Pro
				260					265					270	Phe
	Lys	Gly	Asp	Asp	Ile	Thr	Met	Val	Leu	Ile	Leu	Pro	Lys	Pro	Glu
			275					280					285		Lys
	Ser	Leu	Ala	Lys	Val	Glu	Lys	Glu	Leu	Thr	Pro	Glu	Val	Leu	Gln
		290					295					300			Glu
	Trp	Leu	Asp	Glu	Leu	Glu	Glu	Met	Met	Leu	Val	Val	His	Met	Pro
	305					310					315				Arg
	Phe	Arg	Ile	Glu	Asp	Gly	Phe	Ser	Leu	Lys	Glu	Gln	Leu	Gln	Asp
				325						330					335
	Gly	Leu	Val	Asp	Leu	Phe	Ser	Pro	Glu	Lys	Ser	Lys	Leu	Pro	Gly
			340						345					350	Ile
	Val	Ala	Glu	Gly	Arg	Asp	Asp	Leu	Tyr	Val	Ser	Asp	Ala	Phe	His
			355			</									

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Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys  
 420 425 430

&lt;210&gt; 93

&lt;211&gt; 430

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
 synthetic construct

&lt;400&gt; 93

Ser Pro Val Asp Ile Cys Thr Ala Lys Pro Arg Asp Ile Pro Met Asn  
 1 5 10 15  
 Pro Met Cys Ile Tyr Arg Ser Pro Glu Lys Lys Ala Thr Glu Asp Glu  
 20 25 30  
 Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr Asn Arg Arg Val Trp Glu  
 35 40 45  
 Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr Gln His Leu  
 50 55 60  
 Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser Pro Leu Ser  
 65 70 75 80  
 Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn Asp Thr  
 85 90 95  
 Leu Gln Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser Glu Lys  
 100 105 110  
 Thr Ser Asp Gln Ile His Phe Phe Phe Ala Lys Leu Asn Cys Arg Leu  
 115 120 125  
 Tyr Arg Lys Ala Asn Lys Ala Ser Lys Leu Val Ser Ala Asn Arg Leu  
 130 135 140  
 Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Thr Tyr Gln Asp Ile Ser  
 145 150 155 160  
 Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe Lys Glu Asn  
 165 170 175  
 Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn Lys Thr  
 180 185 190  
 Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn Glu Leu  
 195 200 205  
 Thr Val Leu Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu Trp Lys  
 210 215 220  
 Ser Lys Phe Ser Pro Glu Asn Thr Arg Lys Glu Leu Phe Tyr Lys Ala  
 225 230 235 240  
 Asp Gly Glu Ser Cys Ser Ala Ser Met Met Tyr Gln Glu Gly Lys Phe  
 245 250 255  
 Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln Val Leu Glu Leu Pro Phe  
 260 265 270  
 Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys Pro Glu Lys  
 275 280 285  
 Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu Gln Glu  
 290 295 300  
 Trp Leu Asp Glu Leu Glu Met Met Leu Val Val His Met Pro Arg  
 305 310 315 320  
 Phe Arg Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln Asp Met  
 325 330 335  
 Gly Leu Val Asp Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro Gly Ile  
 340 345 350  
 Val Ala Glu Gly Arg Asp Asp Leu Tyr Val Ser Asp Ala Phe His Lys  
 355 360 365  
 Ala Phe Leu Glu Val Asn Glu Gly Ser Glu Ala Ala Ala Ser Thr  
 370 375 380



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Ala	Val	Val	Ile	Ala	Gly	Arg	Ser	Leu	Asn	Pro	Asn	Arg	Val	Thr	Phe
385					390					395					400
Lys	Ala	Asn	Arg	Pro	Phe	Leu	Val	Phe	Ile	Arg	Glu	Val	Pro	Leu	Asn
				405					410					415	
Thr	Ile	Ile	Phe	Met	Gly	Arg	Val	Ala	Asn	Pro	Cys	Val	Lys		
			420					425					430		